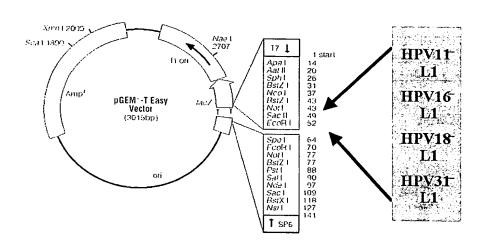
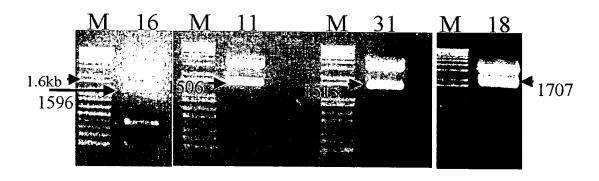
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Fig. 1

(A)



(B)



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	1	10	20	30	40	50	60	70	80	90	100	110	120	130
RF402678 HPV16 Consensus	HIULKU	GI GHL I fill	HIIIHLHILI.	THOST LIBIT LEGS	HIGH RETSRI	MACCACCIA	ABCCITTAC	CATATTTTTTT CATATTTTTTTT CATATTTTTTTT	TERCRITETES	CITYCCCTC	TOCTCOCCC	COCTCTCTO	TTCCCTCCTC	TCCCCC
	131	140	150	160	170	190	190	200	210	220	230	240	250	260
AF 402678 HPV16 Consensus	IHILIH	MUU1161HH	benebulan libi	HIBIGITEER	LITERTARRE	ITATATTATC	ATGEAGGAAN	ATCCAGACTA CATCCAGACTA CATCCAGACTA	FITCHACTTO	COCOTCCCT	TTTTCCTOT	100000 CCT	TOTAL TARGET	
	261	270	280	290	300	310	320	330	340	350	360	370	380	390
AF402678 HPV16 Consensus								1116611110 1116611110						
	391	400	410	420	430	440	450	460	470	480	490	500	510	520
RF 402678 HPV16 Consensus								TGGATGACAC TGGATGACAC TGGATGACAC						
	521 	530	540	550	560	570	580	590	600	610	620	630	640	650
RF402678 HPV16 Consensus	CTATEG							GGGCARAGGA GGGCARAGGA GGGCARAGGA						
	651 		670	680	690	700	710	720	730	740	750	760	770	780
AF402678 HPV16 Consensus								TTACAGGCTA TTACAGGCTA TTACAGGCTA						
	781	790	800	810	820	830	840	850	860	870	880	890	900	910
RF402678 HPV16 Consensus								TTGTTRGRCA TTGTTRGRCA TTGTTRGRCA						
	911	920	930	940	950	960	970	980	990	1000	1010	1020	1030	1040
RF402678 HPV16 Consensus		CTGGGTCTR		RGCCRGTTCR	RATTATTTTC	CTACACCTA	GTGGTTCTAT	GGTTRCCTCT GGTTRCCTCT GGTTRCCTCT	GATGCCCAAA	TATTCRATA	RCCTTATTGE	TTACAACGAC	GERERGGGEER GERERGGGEER	
RF402678				1070	1080	1090	1100	1110	1120	1130	1140	1150	1160	1170
HPV16 Consensus	TGGCRT	TTGTTGGGG	TAACCAACTA	TTTGTTACTG				TCATTATGTG TCATTATGTG TCATTATGTG						
	1171		1190	1200	1210	1220	1230	1240	1250	1260	1270	1280	1290	1300
RF402578 HPV16 Consensus								ACGTTATGTC ACGTTATGAC ACGTTATGAC						
	1301		1320	1330	1340	1350	1360	1370	1380	1390	1400	1410	1420	1430
AF402678 HPV16 Consensus								ARARCATACA BRANKCATACA BRANKCATACA						
	1431	1440	1450	1460	1470	1480	1490	1500	1510	1520	1530	1540	1550	1560
RF402678 HPV16 Consensus								IGGATTTAAGG IGGATTAARGG IGGATT A ARGG						
	1561	1570	1580	1590593										
AF402678 HPV16 Consensus	TETRER	RETGETRARI	CGCRARARAC CGCRARARAC CGCRARARAC	GTAAGCTG										

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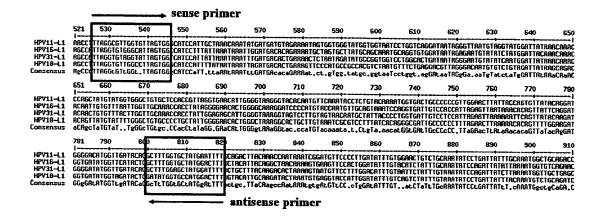
	1	10	20	30	40	50	60	70	80	90	100	110	120	130
J04353 HPV31_L1 Consensus								TGTRAGEACGG TGTRAGEACGG TGTRAGEACGG						
	131	140	150	160	170	180	190	200	210	220	230	240	250	260
J04353 HPV31_L1 Consensus								RRGETGTCRGG RRGETGTCRGG RRGETGTCRGG						
	261 	270	280	290	300	310	320	330	340	350	360	370	380	390
J04353 HPV31_L1 Consensus	TGATE							TRGGTCGCGGG TRGGTCGCGGG TRGGTCGCGGG						
	391	400	410	420	430	440	450	460	470	480	490	500	510	520
J04353 HPV31_L1 Consensus	GAAA	CICIRATA						TTATRARCARA TTATRARCARA TTATRARCARA						
	521 	530	540	550	560	570	580	590	600	610	620	630	640	650
J04353 BPV31_L1 Consensus	STCCI	TGTRGTRA	CRATECTATTE CRATECTATTE CRATECTATTE	CCCCTGGTGF CCCCCTGGTGF CCCCCTGGTGF	ALLEGICTICS ALLEGI	ATTREBATTRE ATTREBATTRE ATTREBATTRE	WARRATTCA WARRATTCA WARRATTCA	GTTATACARGA GTTATAGARGA GTTATACARGA	TGGGGATATGG TGGGGATATGG	TTGATACAG TTGATACAG TTGATACAG	CTTTEGREC CTTTEGREC	TRIGGATTIT TRIGGATTIT TRIGGATTIT	RCTGCTTTACE RCTGCTTTACE RCTGCTTTACE	AGACRE AGACRE AGACRE
	651 	660	670	680	690	700	710	720	730	740	750	760	770	780
J04353 HPV31_1.1 Consensus	TRRAF							TGGTTGCTGRG TGGTTGCTGRG TGGTTGCTGAG						
	781 	790	800	810	820	830	840	850	860	870	880	890	900	910
J04353 HPV31_L1 Consensus	min	TRATAGATI	CREGCRCEST 1 CREGCRCEST 1 CREGCRCEST 1	GGTGARTCGC GGTGARTCGC GGTGARTCGC	TECCTACTS TECCTACTS	ACTTATATATI ACTTATATATI ACTTATATATI	ARRGECTO BARGECTO BARGECTO	CGGTTCRRCAG CGGTTCRRCAG CGGTTCRRCRG	TRETTTREET TRETTTREET TRETTTREET	RACAGTACA RACAGTACA RACAGTACA	RCTTTCCTA RCTTTCCTA RCTTTCCTA	ACC TAGEGGI ACC TAGEGGI ACC TAGEGGI	TCCATGATTA TCCATGATTA TCCATGATTA	CTTCAG CTTCAG CTTCAG
	911	920	930	940	950	960	970	980	990	1000	1010	1020	1030	1040
J04353 HPV31_L1 Consensus								TGTTGGGGCRA TGTTGGGGCRA TGTTGGGGCRA						
	1	1050	1060	1070	1080	1090	1100	1110	1120	1130	1140	1150	1160	1170
J04353 HPV31_L1 Consensus								GTGAGGAATTTI GTGAGGAATTTI GTGAGGAATTTI						
	1	1180	1190	1200	1210	1220	1230	1240	1250	1260	1270	1290	1290	1300
J04353 HPV31_L1 Consensus								CTCRGGTTCTT CTCRGGTTCTT CTCRGGTTCTT						
	1	1310	1320	1330	1340	1350	1360	1370	1380	1390	1400	1410	1420	1430
J04353 HPV31_11 Consensus								ARGTTTTCTGC RAGTTTTCTGC ARGTTTTCTGC						
	1	1440	1450	1460	1470	1490	1490	1500	151812					
MPV31_11	HCBIC	CIHAMILIE	OPPOLITIES FRA	ACGTRATACA	CCCTCR6CA	TETREFACTAC	ALL BELLEVI	RRCGTANAARA RACGTAAAARA RACGTAARAAA	200000720					

	1	10	20	30	40	50	60	70	80	90	100	110	120	130
MC_001525 HPV11_L1 Consensus	ніыц	LLGIA.CTR	GLUSIOLIUS POLI	RGTATATGTG	CILLILLE	ALLLALLALL	CRACETTI	CTTCCCACCC	TOTOTOTOT	7000CCC0CC	DOCOTOTYTO	TEGTECCOCCO	GTTCTAGACTI GTTCTAGACTI	
	131	140	150	160	170	180	190	200	210		230	240	250	260
MC_001525 HPV11_L1 Consensus	luubh	LHILLMIN	FINCILIBIL	100000011110	THE BEHALL	ISTRUCTARRE	GIETTIG	GATAICAATAI	PRODUCT CYTY	DOCCTOCTCT	TCCCCCCTCCT	DOCCOCTTTC	CATTACCTGATI CATTACCTGATI CATTACCTGATI	COTOTOT
	261	270	280	290	300	310	320	330	340	350	360	370	380	330
MC_001525 HPV11_L1 Consensus													GATGTAGARA GATGTAGARA GATGTAGARA	
	391	400	410	420	430	440	450	460	470		490	500	510	520
HC_001525 HPV11_L1 Consensus	GGGTA												RGGGTACACRI RGGGTACACRI RGGGTACACRI	
	521 I	530	540	550	560	570	580	590	600	610	620	630	640	E50
HC_001525 HPV11_L1 Consensus	RTACC	TETGTACA											RACCRATARA BACCRATARA BACCRATARA	
	651 	660	670	680	690	700	710	720	730	740	750	760	770	780
NC_001525 HPV11_L1 Consensus	TCCCC												RGACACTTTT RGACACTTTT RGACACTTTT	
	781 	790	800	810	B20	830	840	850	860	870	880	890	900	910
MC_001525 HPV11_i1 Consensus													CTTCAGAGGC1 CTTCAGAGGC1 CTTCAGAGGC1	
	911	920	930	940	950	960	970	980	990	1000	1010	1020	1030	1040
MC_001525 HPV11_L1 Consensus													ATETOCATOTO ATETOCATOTO ATETOCATOTO	
	1041		1060	1070	1080	1090	1100	1110	1120	1130	1140	1150	1150	1170
MC_001525 HPV11_L1 Consensus													GCCTATATACE GCCTATATACE GCCTATATACE	
	1171	1180	1190	1200	1210	1220	1230	1240	1250	1260	1270	1280	1290	1300
MC_001525 HPV11_L1 Consensus													CACCTGARARE CACCTGARARE CACCTGARARE	
	1301	1310	1320	1330	1340	1350	1360	1370	1380	1390	1400	1410	1420	1430
MC_001525 HPV11_L1 Consensus													RGGACGGRCG1 RGGACGGRCG1 RGGACGGRCG1	
	1431		1450	1460	1470	1480	1490	15045						
NC_001525 HPV11_L1 Consensus	TREAG	GTATARAG	GCCCRGCTGT	TGTCTRRGCCC	TOTACRECO	CCCRRRCGARI CCCRRRCGRRI CCCRRRCGARI	RAPORTACY	"ARRRTTRARK"	MG 2RM					

	1	10	20	30	40	50	60	70	BO	90	100	110	120	130
NC_001357 HPV1BL1-U	ATGTO	SCCTSTRTRC	ACGGGTCCTG	TATTACATT	ACCATETAC	TRECTETATA	TEGECERTTE	TATCACCCAC	GGCCCCT6CC	TCTACACAGT				i
HPV1BL1-L Consensus			RCGGGTCCTGF RCGGGTCCTGF	iiiii inchii	nicon i c i nci	LILLIGIA	IGGLECHIIG	HILMLLICHL	HECCUCIECC	TETRERERGI	ATATTGGTATA	ACATEGTACA	C ATTATTATT	TGTGGCC
_	131	140	150	160	170	180	190	200	.GC.CC.1GC. 210	220	#1HT1G5TRT1	9240	CATTATTATT 250	TGTGGCC 260
MC_001357	RITRI	ATTATETA	TTCCTRRGRRF	CGTRAACGI	GTTCCCTAT	TTTTTTGCRG	ATGGCTTTGT	GECEGCCTAS						ï
HPV18L1-L Consensus						· · · · · · · · · · · · · · · · · · ·		uucuucc i na	I GINCHINI I TILCI	PINIMICITO	CHECTECTIC	G I GGCRRIGE	IGT TGT RAAT AS	CCCATGA
	261	270	TTCCTRRGRRF 280	290	300	310	320	330	16HCRH1RCC 340	350 350	CRECTECTTE: 360	GTGGCARGA 370		
NC_001357 HPV18L1-U	TIBIO	TGACTCCCA	CARGCATATTI	THTCHTGCT	GGCRGCTCTI	RGATTATTAR	CTGTTGGTRA						380	390
HPV18L1-U HPV18L1-L Consensus					addition of the	acomi in a ci inne	CIGIIGOINA	CUNINGER	HOUR I ILLIU	166 LPR	CHATAASCAS	ATATTCCTA	RAGGTTTCTGC	ATRCCAA
	391	400	CARGCATATTT	420	430	440	#50	460	RGGGTTCCTG 470	CRGGTGGTGG	CARTRASCAGO 490			
NC_001357	TRIRE	AGTATTTRO	GGTGCRGTTRC	CTGRCCCAA	ATRASTTICA	STITRECTER		******				500 DCTCC000T	510	520
HPV18L1-U HPV18L1-L Consensus						JI I I I I I I I I I I I I I I I I I I	incinaini i	in innicitie	WHICH HELD	111186161666	ecciei acia	RIGT GGRART	TEECCETEET	CAGCCTT
Consensus	521	#16TH1TH6	GGTGCAGTTAC 540	SSO	9788877760 560	STITACCTGA: 570	TACTAGTATT SAO						TEGCCGTGGT	CRGCCTT
NC_001357	TREGI	GTTGGCCTT	RGTGGGCRTCC	RTTTTRTRR	TRRATTERA	FOCOCTEON	CTICCOIC	590	600	E10	620	630	640	650
HPV18L1-U HPV18L1-L	-					CONCINCTORNI	in a recent of	CCGCCRCG I C	INNIGITICI	MOGNEGIIN	فا	HUI GINGHI	THTHHISCHISH	CHCHGTT
Consensus	TRGG1	660	RGTGGGCATCC 670	RATATTTE: OSBA	TRAATTAGAT						G			
NC_001357	1		TGCCCCTGCT			700	710	720	730	740	750	760	770	780 1
HPV18L1-U HPV18L1-L						DEROGLIK. 1 OC	-11011111111111	occirc.iiin	CHUNGGGG		I I THIGHNET TH	KAHACACAG	TTTTGGAAGA	FEGTERT
Consensus	781	790	800	R10										
HC_001357	1		TATGGTGCCA		820 CTOCOTTOCO	830 OCCTOC TOO	840	850	860	870	880	890	900	910
#PV18L1-U #PV18L1-L			ourocca		o inchi i del	WHOM I THE I AME	TI G FORISS I PR	CCRT FORMER	HIGICHEIC	HILLETHAN	TATCCTGATTA	ITTTRCARAT	GTCTGCRGATO	CTTATG
Consensus														
	044	***												
NC 001357	911 	320 TCC015111	930	940	950	960	970	980	990	1000	1010	1020	1030	1040
NC_001357 HPV18L1-U HPV18L1-L	1		930 ITTTGCTTRCG											
HPV18L1-U	GGGAT	TCCATGTTT	TTTGCTTRCG	GCGTGAGCA	GCTTTTTGCT	REGCRITTI	GGAAT RGAGI	CRESTACTATI						
HPV18(1-() HPV18(1-L Consensus	1041	TCCATGTTT	1060	GCGTGAGCA 1070	GCTTTTTGCT	AGGCATTTT1	TGGRATAGAGI	CRESTACTATE	SEGTENCECTE	1130	CTTATATATI	RANGGCACA 1150	GGTATGCCTGC	TTCRCC
HPV18L1-U HPV18L1-L Consensus NC_001357 HPV18L1-U HPV18L1-L	1041	TCCATGTTT	TTTGCTTRCG	GCGTGAGCA 1070	GCTTTTTGCT	AGGCATTTT1	TGGRATAGAGI	CRESTACTATE	SEGTENCECTE	1130	CTTATATATI	RANGGCACA 1150	GGTATGCCTGC	TTCRCC
HPV18L1-U HPV18L1-L Consensus NC_001357 HPV18L1-U	1041 TGGCR	TCCATGTTT 1050 GCTGTGTGTA	1060	GCGTGAGCA 1070 CCARGTGGC	1080	1090	1100 CCRGTTGTTT	1110	1120	1130	CTTATATATI	RANGGCACA 1150	GGTATGCCTGC	TTCRCC
HPV181.1-U HPV181.1-L Consensus HC_001357 HPV181.1-U LCONSENSUS HC_001357	1041 TGGCR	1050 GCTGTGTGTGT	1060 1071 TETECETEN	1070 CCRRGTGGC	1080 TCTATTGTTR	1090 ECCTCTGACTO	1100 CCRGTTGTTT	1110 TRATABACCET 1240	1120 TRITISGITACE	1130 ITANGGCACAG	1140 SGGTCRTARCR	1150 HTGGTGTTT	1160 GCTGGCATAAT	1170 1170 ICARTTR
HPV18L1-U HPV18L1-L Consensus MC_001357 HPV18L1-U HPV18L1-U MC_001357 HPV18L1-U HPV18L1-U	1041 TGGCR	1050 GCTGTGTGTGT	1060	1070 CCRRGTGGC	1080 TCTATTGTTR	1090 ECCTCTGACTO	1100 CCRGTTGTTT 1230 RCRCTGTTCTC CRGTCTC	1110 IRATRANCENT 1240 ECTGTRECTGE	1120 INTEGTACE 1250 GCRATATEGT	1130 ITANGGCACHE 1250 GCTACCARAT	1140 GGTCATARCA 1270 TTRRGCRGTA	1150 RTGGTGTTT 1280 TAGGREGACA	1160 GCTGGCATANT 1290 TGTTGAGGANT	1170 1170 1170 1170 1170 1300
HPV18L1-U HPV18L1-L Consensus NC_001357 HPV18L1-U Consensus NC_001357 HPV18L1-U	1041 TGGCR	1050 SCTETETETE 1180 TRCTETEGTE	1060 HTTETCCCTCT 1190	1070 CCRRGTGGC 1200 CCRGTRCCR	1080 TCTATTGTTR 1210 RTTTRACRAT	1090 ECCTCTGACTO 1220 ATGTGCTTCT	1100 CCRGTYGTT 1230 RCRCRGTCTC CRGTCTC	1110 TRATABACCAT 1240 CCTGTRCCTGC	1120 INTEGRATACE 1250 GCRATATGAT GCRATATGAT	1130 ITANGGCACAE 1260 GCTACCARAT	1140 IGGTCATARCA 1270 ITTRAGCAGTA	1150 RTGGTGTTT 1280 TAGGREGACA	1160 GCTGGCATAAT	1170 1170 1170 1170 1170 1300
HPV1811-U HPV1811-U Consensus NC_001357 HPV1811-U Consensus NC_001357 HPV1811-U HPV1811-U Consensus	1041 1060RT 1060CR	1050 GCTGTGTGT6 1180 TACTGTGGT6	1060 HTTCTCCCTCT 1190 IGRTRCCACTC	1070 CCARGTGGC 1200 CCAGTACCA 1330	1080 TCTATTGTTR 1210 RTTTBACRAT	1090 ECCTCTGACTO 1220 ATGTGCTTCT	1100 CCRGTTGTTT 1230 RCRCRGTCTC CRGTCTC CRGTCTC 1360	1110 IRATRARICCAT 1240 CCTGTRCCTGG CCTGTRCCTGG	1120 INTEGRATACE 1250 GGCRATAGET GGCRATAGET GGCRATAGET 1380	1130 ITANGGCACHE 1260 GCTACCARATI GCTACCARATI	1140 SGGTCATARCA 1270 TTTRISCAGTA TTRISCAGTA TTRISCAGTA	1150 ATEGTETTT 1290 TRECHERCE TRECHERCE TRECHERCE TRECHERCE TRECHERCE TRECHERCE TRECHERCE TRECHERCE TRECHERCE	1160 GCTGSCHTANT 1290 TGTTGAGGANT TGTTGAGGANT TGTTGAGGANT	1170 1170 1300 1300 REGRITE REGRITE REGRITE 1430
HPV1811-1. Consensus NC_001357 HPV1811-0 HPV1811-1 Consensus NC_001357 HPV1811-1 Consensus NC_001357 HPV1811-1 HPV1811-1 HPV1811-1 HPV1811-1	1041 1060R 1171 1171 1171 1301	1050 1180 TACTGTGGTF 1310	1060 11100 11190 GRITACCACTC 1320 AGTIGGIGGAC	1070 CCARSTGSC 1200 CCAGTACCA 1330 TATTACTTA	1080 TCTATTGTTR 1210 RTTTBACAGT 1340 RRACTGCAGGT	1090 ECCTCTGACTO 1220 ATGTGCTTCT 1350 GTTATGTCCT	1100 LCCAGTTGTTT 1230 RCACAGTCTC CAGTCTC CAGTCT CAGTC	1110 IRRITARRICCAT 1240 CONTROL TO THE CONTROL TO	1120 ATTGGTTACA 1250 SGCRATATGAT GGCRATATGAT 1390 RGTATTTIRG	1130 TRANGGEACHE 1260 GETACEARNI GETACEARNI 1390 REGENTTEGRA	1140 GGGTCATANCA 1270 TYRNGCAGTA TYRNGCAGTA 1400	1150 RTGGTGTTT 1290 TRGCRGGCR TRGCRGCR TRGCRGCR 1410 CCCCCCCCCC	1160 CTGGCATART 1290 TGTTGAGGART TGTTGAGGART 1420 CCARCTRCTRC	1170 1300 INTERRITE RESERVE TERRITERISERVE TERRITER
HPV1811-U HPV1811-U Consensus MC_001357 HPV1811-U Consensus MC_001357 HPV1811-U HPV1911-L Consensus	1041 TGGCR 1171 TTGT 1301 TGCRG TGCRG	1050 CETETETETE 1180 TACTETEGETE 1310 TITALLITE T	1060 11190 11320 RETTETETEC	1070 CCARGTGGC 1200 CCAGGTGCCA 1330 THITRCTTIC THITRCTTIC	1080 TCTATTGTTR 1210 RTTTBACRAT 1340 RRCTGCRGRT	1090 1090 1220 ATGRIGATIC 1350 GYTATGRIGAT GYTATGRI	1100 1230 1230 1230 1230 1230 1230 1230 1230 1230 1230 1360 1360 1360 1361 1360	1110 IRATARACCAT 1240 LEGGRECISC LEGGRECISC LIGHRECISC LIGHRESIST LIGHRIPS LIGH	1120 INTEGRATAGE 1250 GEORATHAGE GEORATHAGE GEORATHAGE 1380 GRATHITING GRATHITING GRATHITING GRATHITING GRATHITING	1130 TRAGGERERA 1260 GETACERRAI GETACERRAI 1390 REGATTEGRA	1140 GGGTCATANCA 1270 TYRNGCAGTA TYRNGCAGTA 1400	1150 RTGGTGTTT 1290 TRGCRGGCR TRGCRGCR TRGCRGCR 1410 CCCCCCCCCC	1160 CTGGCATART 1290 TGTTGAGGART TGTTGAGGART 1420 CCARCTRCTRC	1170 1300 INTERRITE RESERVE TERRITERISERVE TERRITER
HPY181.1-U CONSENSUS MC_001357 HPY181.1-U HPY181.1-U HPY181.1-U HPY181.1-U SPY181.1-U CONSENSUS MC_001357 HPY181.1-U CONSENSUS MC_001357 HPY181.1-U CONSENSUS MC_001357 HPY181.1-U	1041 106CR 1171 1171 1171 1171 1171 1171 1171 11	1050 1050 1180 1780 1790 1790 1790 1790 1790 1790 1790 179	1060 1060 11161CCCCTCT 1190 IGRITACESCTC 1320 IGRITGITGITE RETTIGITETE RETTIGITETE RETTIGITETE RETTIGITETE RETTIGITETE RETTIGITETE RETTIGITETE RETTIGITETE	1070 CCRRGTGGCR 1200 CCRGTGCCR 1330 TRITICCTTIC TRITICCTTIC	1080 ICTATTGTTR 1210 BITTRACRAT 1340 RACTGCAGAT RACTGCAGAT RACTGCAGAT 1470	1090 ECCTCTGGCTC 1220 ATGTGCCTCC 1350 GTTATGTCCT GTTATGTCCT GTTATGTCCT 1480	1100 CCRGTTGTTT 1230 RCRCRGTCTC CRGTCTC CRGTCTC ATRITICATRC RTRITICATRC RTRITICATRC RTRITICATRC RTRITICATRC RTRITICATRC RTRITICATRC RTRITICATRC RTRITICATRC	1110 IRRITARROCCAT 1240 CETETRECTEG CETETRECTEG CETETRECTEG CETETRECTEG 1370 GETETREATREG CETETRECTEG CETETRECTEG CETETRECTEG CETETREATREG CETETREAT	1120 ATTEGTTACA 1250 SECRATATEAT SECRATATEAT 1380 AGTATTTACA 1380 AGTATTTACA 1510	1130 TRANGGEACHE 1250 GETRICERRA GETRICERRA 1330 REGRIT TEGRA REGRIT TEGRA 1520	1140 SEGECATARCA 1270 THRESCAGE THRESCAGE 1400 EXTHESIGNET EXTHESIGNET EXTHESIGNET EXTHESIGNET EXTHESIGNET 1530	1150 ATGGTGTTT 1280 TRGCRGRCR TRGCRGRCR 1410 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	1160 6CTGGCGTAN1 1290 TGTTGGGGATT TGTTGGGGAT 1420 CCARCTRETAS CCARCTRETAS CCARCTRETAS 1550	1170 1200 1300 REGATTA 1300 REGATT RE
#FY18.1-U Consensus MC.001357 #FY18.1-U #FY18.1-U #FY18.1-U #FY18.1-L Consensus MC.001357 #FY18.1-L Consensus MC.001357 #FY18.1-L Consensus	1041 1041 1TGGCR 1171 1TGT 1301 15CRG 1GCRG 1GCRG 1431 1	1050 1180 TACTGTGGTF 1310 THENTITIC THENTITIC 1440 CREATEGTF	1060 1060 11190 INTERCECTET 1190 INTERCECTET 1320 RETIGITETE RETIGITETE 1450 1450	1070 CCARGTGGC 1200 CCAGTACCA 1330 TATTACTTIC TATTACTTIC TATTACTTIC 1460 TTGCTATTACTATTACTATTACTATTACTATTACTATTACTATTACTATTACTATTACTATTACTATTACTATTACTATTACTATTACTAC	1080 ICTATTGTTR 1210 RETTERACHET 1340 RECTGCREAT 1347 1340 RECTGCREAT 1470 1470	1090 ECCTCTGACTC 1220 ATGTGCTTCT 1350 GTHRIGTCT GTHRIGTCT 1480 RGGHRGCTGCT	1100 CCRGTTGTTT 1230 RCRCRGTCTC CRGTCTC 1360 RTRITCRIRG RTRITCRIRG RTRITCRIRG RTRITCRIRG ACCCGCTGRR	1110 IRRITARROCCAT 1240 CETETRECTEC ETETRECTEC ETETRECTEC TATORNAMENTAGE TATORNAM	1120 1250 1250 1250 GGCRATHIGHT GGCRATHIGHT GGCRATHIGHT 1380 RGTHITTHR RGTHITTHR RGTHITTHR RGTHITTHR LGTHITTHR LGTHITHR LGTHITHR	1130 TRANGECACHE 1250 GCTACCARAN GCTACCARAN GCTACCARAN 1330 REGATTEGRAR REGATTEGRAR REGATTEGRAR 1520	1140 SGETCATIONER 1270 THRISCINGTH THRISCINGTH THRISCINGTH 1400 ECTHISGENGTH ECTHISGENGTH ECTHISGENGTH 1530 TGGGRATGTISG	1150 ATGGTGTTT 1280 TRIGGTGGTGTT 1280 TRIGGTGGTG TRIGGTGGCG TRIGGTGGCG 1410 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	1160 GCTGGCATAA1 1290 TGTTGAGGAA1 TGTTGAGGAA1 1420 CCCARCTACTAC CCCARCTACTACTACTACTACTACTACTACTACTACTACTACTAC	1170 1300 1300 REGRITA REGRITARISHIT REGRITARISHIT 1430 RETTEGRITARISHIT 1430 RETTEGRITARISHIT 1550 TERREGRITARISHIT
#F7181.1-U Ensensus MC_001357 #F7181.1-U Ensensus MC_001357 #F7181.1-U Ensensus MC_001357 #F7181.1-U F7181.1-U F7181.1-U Ensensus MC_001357	1041 TGGCR 1171 TTGGT 1301 TGCRG TGC	1050 1180 TACTOTOGIST 1310 THATTITIC 11440 CONTRICTORY CONTRICT	1060 1190 1320 ARGITIGITATE	1070 CCRRGTGGC 1200 CCRGTRCCRI 1330 TRITRCTTI TRITRCTTI TRITRCTTI 1460 GUIGCURITE GUIGCURITE GUIGCURITE GUIGCURITE GUIGCURITE	1080 ICTATTGTTR 1210 RETTRACRATT 1340 RACTGCAGAT 1470 1470 1470 AGCTGTCARAR ACCTGTCARAR	1090 1090 1220 ATERISCITET 1350 GITATGICET GITATGICET 1480 AGGATGICET	1100 CCRGTTGTTT 1230 RCRCRGTCTC CRGTCTC 1360 RTRITCRIRG RTRITCRIRG RTRITCRIRG RTRITCRIRG ACCCGCTGRR	1110 IRRITARROCCAT 1240 CETETRECTEC ETETRECTEC ETETRECTEC TATORNAMENTAGE TATORNAM	1120 1250 1250 1250 GGCRATHIGHT GGCRATHIGHT GGCRATHIGHT 1380 RGTHITTHR RGTHITTHR RGTHITTHR RGTHITTHR LGTHITTHR LGTHITHR LGTHITHR	1130 TRANGECACHE 1250 GCTACCARAN GCTACCARAN GCTACCARAN 1330 REGATTEGRAR REGATTEGRAR REGATTEGRAR 1520	1140 SGETCATIONER 1270 THRISCINGTH THRISCINGTH THRISCINGTH 1400 ECTHISGENGTH ECTHISGENGTH ECTHISGENGTH 1530 TGGGRATGTISG	1150 ATGGTGTTT 1280 TRECREGEC TRECREGEC 1410 CCCCCCCCCC CCCCCCCCCCCCCCCCCCCCCC	1160 GCTGGCATAA1 1290 TGTTGAGGAA1 TGTTGAGGAA1 1420 CCCARCTACTAC CCCARCTACTACTACTACTACTACTACTACTACTACTACTACTAC	1170 1300 1300 REGRITA REGRITARISHIT REGRITARISHIT 1430 RETTEGRITARISHIT 1430 RETTEGRITARISHIT 1550 TERREGRITARISHIT
#F7181.1-U F7181.1-U	1041 TGGCRG 1171 TTTGT 1301 TGCRG 16CRG 1431 TGGRG 16GRTE 1561	1050 1180 1310 1181111111 114111111 1440 CETATECTTT CETATECTTT CETATECTTT CETATECTTT CETATECTTT CETATECTTT CETATECTTT CETATECTTT CETATECTTT 1570	1060 1060 1190 1190 1320 AGTIGICIAC RETIGITAC	1070 CCARGIGGC 1200 1200 1330 THITECTIFE THITECTIFE THITECTHITE THITECTHITE GITECTHITE GITECTHITE GITECTHITE GITECTHITE GITECTHITE GITECTHITE THISCITHITE 1590	1080 TCTATTGTTR 1210 RTTTRACRATT 1340 RRCTGCRAGAT RRCTGCCAGAT RRCTGCAGAT RRCTGCCAGAT RRCTGCCAGAT RRCTGCAGAT RRCTGCCAGAT RRCTGCAGAT RRCTGCAGA	1090 ECCICTORCIC 1220 ATGRECTECT 1350 GTHRIGICET GTHRIGICET GTHRIGICET ARBO ARGANICETEC ARGANICETEC 1510	1100 1230 1230 1230 1230 1230 1230 1230	1110 1240 1240 1250 1250 1370 1370 1370 1370 1370 1370 1370 137	1120 1250 1250 1250 1250 1250 1250 1250	1130 TRANGGENERA 1260 GETACCARAN TASO GETACCARAN TASO TOTALARAN TOTALAR	1140 GGGTCATAMEN 1270 THRESCHOTT	1150 ATGGTGTTT 1290 TRICARGACA TRICAGRACA TRICAGRACA 1410 CCCCCCCCCC CCCCCCCCCCCCCCCCCCCCCCC	1160 GCTGGCRITANI 1290 TGTTGGGGRRIT TGTTGGGGRRIT TGTTGAGGGRRIT TGTTGAGGGRRIT 1420 CCRRCTRCTRGCTGCCCRRCTRGTGGCCCCRRCTRGTGGCCCCRRCTRGTGGCCCCRRCTRGTGGCCCRRCTRGTGGCCCRRCTRGTGGCCCRRCTRGTGGTGGCCCRRCTRGTGGTGGCCCRRCTRGTGGTGGCCCRRCTRGTGGTGGTGGGGGTGTGCTGGGGGGGTGTGCTGGGGGGGG	1170 1170 1288TT8 1300 REGRIT REGRIT REGRIT REGRIT REGRIT REGRIT TITEGE
#F7181.1-U Ensensus MC_001357 #F7181.1-U Ensensus MC_001357 #F7181.1-U	1041 TGGCR 1171 1301 1301 15CRG TGC	1050 1180 170 171 171 171 171 171 171 171 171 17	1060 1190 1320 1320 1450 1450 16 HEART FIGURE 1450 16 HEART FIGURE 15 HEART FI	GCGTGAGCA 1070 CCARGTGGC 1200 CCAGGTACCAC 1330 TRITACTIT TR	1080 TCTATTGTTR 1210 RTTTRACART 1340 RRCTGCAGAT RRCTGCAGAT RRCTGCAGAT 1470 ACCTGTCAGAT RCCTGTCAGAT R	1090 1220 1220 ATGTGCTTCT 1350 GTTATGTCCT GTTATGTCCT 1480 PROGRATECTEC PROGRATECTEC PROGRATECTEC REGATECTEC 1510 ATTECGTCCCC	1100 1230 REGERTRETCH CARGITET	1110 1240 CCTGTRCCTGT CCTGTRCCTGC CCTGTRCCTGC CCTGTRCCTGC CTGTRCCTGC CTGTRCCTGC CTGTRCCTGC CTGTRCCTGC CTGTRCCTGC CTGTRCCTGC CTGTRCCTGC CTGTRCATRCGC CTGTRCATRCCC	1120 1250 1250 1250 1250 1250 1250 1250	1130 TRANGECACHE 1260 GCTACCHRAIL GCTACCHRAIL 1390 AGGATT GGAR AGGATT GGAR 1520 GTTACCHRAIL 1520 GTTACCHRAIL 1520 GTTACCHRAIL 1520 GTTACCHRAIL 1520 GTTACCHRAIL 1520 GTTACCHRAIL 1550 GCTCCATCTG	1140 SGGTCRTANCR 1270 THRISCAGUR	1150 1200 176CRETTTI 1200 176CREGRER 1410 CCCCCCCCCCC CCCCCCCCCCCCCCCCCCCCCC	1160 GCTGGCATAGAT 1290 TGTTGGGGGAT TGTTGGGGGAT TGTTGGGGGAT 1420 CCRRCTCTGTGTGGGGAT 1420 TGTTGATGGGAT 1420 TGTTGATGGGAT 1420 TGTTGATGGAT 1550 TGTTGAT 1550 TGTTGA	1170 1300 1300 1816HTT 1430 11716HT
#F7181.1-U F7181.1-U	1041 TGGCR 1171 1301 TGCRG TGC	1050 1180 1310 THE	1060 1060 1190 1190 1320 AGTIGICIAC RETIGITAC	GCGTGAGCA 1070 CCARGTGGC 1200 CCAGGTACCAC 1330 TRITACTIT TR	1080 TCTATTGTTR 1210 RTTTRACART 1340 RRCTGCAGAT RRCTGCAGAT RRCTGCAGAT 1470 ACCTGTCAGAT RCCTGTCAGAT R	1090 1220 1220 ATGTGCTTCT 1350 GTTATGTCCT GTTATGTCCT 1480 PROGRATECTEC PROGRATECTEC PROGRATECTEC REGATECTEC 1510 ATTECGTCCCC	1100 1230 REGERTRETCH CARGITET	1110 1240 CCTGTRCCTGT CCTGTRCCTGC CCTGTRCCTGC CCTGTRCCTGC CTGTRCCTGC CTGTRCCTGC CTGTRCCTGC CTGTRCCTGC CTGTRCCTGC CTGTRCCTGC CTGTRCCTGC CTGTRCATRCGC CTGTRCATRCCC	1120 1250 1250 1250 1250 1250 1250 1250	1130 TRANGECACHE 1260 GCTACCHRAIL GCTACCHRAIL 1390 AGGATT GGAR AGGATT GGAR 1520 GTTACCHRAIL 1520 GTTACCHRAIL 1520 GTTACCHRAIL 1520 GTTACCHRAIL 1520 GTTACCHRAIL 1520 GTTACCHRAIL 1550 GCTCCATCTG	1140 SGGTCRTANCR 1270 THRISCAGUR	1150 1200 176CRETTTI 1200 176CREGRER 1410 CCCCCCCCCCC CCCCCCCCCCCCCCCCCCCCCC	1160 GCTGGCATAGAT 1290 TGTTGGGGGAT TGTTGGGGGAT TGTTGGGGGAT 1420 CCRRCTCTGTGTGGGGAT 1420 TGTTGATGGGAT 1420 TGTTGATGGGAT 1420 TGTTGATGGAT 1550 TGTTGAT 1550 TGTTGA	1170 1300 1300 1816HTT 1430 11716HT
##7181.1-U FY181.1-U	1041 10608 1171 1301 15066 15066 15066 15066 1431 1561 1561 171668 171668	1050 1180 1310 1716111110 1716111110 1716111110 1716111110 1716111110 1716111110 1716111110 1716111110 1716111110 1716111110 1716111110 1716111110 1716111110 1716111110 1716111110 1716111110 17161110 1716110 1716110 1716110 17161110 17161110 17161110 1716110 171	1060 1190 1320 1320 1450 1450 16 HEART FIGURE 1450 16 HEART FIGURE 15 HEART FI	GCGTGAGCA 1070 CCARGTGGC 1200 CCAGGTACCAC 1330 TRITACTIT TR	1080 TCTATTGTTR 1210 RTTTRACART 1340 RRCTGCAGAT RRCTGCAGAT RRCTGCAGAT 1470 ACCTGTCAGAT RCCTGTCAGAT R	1090 1220 1220 ATGTGCTTCT 1350 GTTATGTCCT GTTATGTCCT 1480 PROGRATECTEC PROGRATECTEC PROGRATECTEC REGATECTEC 1510 ATTECGTCCCC	1100 1230 REGERTRETCH CARGITET	1110 1240 CCTGTRCCTGT CCTGTRCCTGC CCTGTRCCTGC CCTGTRCCTGC CTGTRCCTGC CTGTRCCTGC CTGTRCCTGC CTGTRCCTGC CTGTRCCTGC CTGTRCCTGC CTGTRCCTGC CTGTRCATRCGC CTGTRCATRCCC	1120 1250 1250 1250 1250 1250 1250 1250	1130 TRANGECACHE 1260 GCTACCHRAIL GCTACCHRAIL 1390 AGGATT GGAR AGGATT GGAR 1520 GTTACCHRAIL 1520 GTTACCHRAIL 1520 GTTACCHRAIL 1520 GTTACCHRAIL 1520 GTTACCHRAIL 1520 GTTACCHRAIL 1550 GCTCCATCTG	1140 SGGTCRTANCR 1270 THRISCAGUR	1150 1200 176CRETTTI 1200 176CREGRER 1410 CCCCCCCCCCC CCCCCCCCCCCCCCCCCCCCCC	1160 GCTGGCATAGAT 1290 TGTTGGGGGAT TGTTGGGGGAT TGTTGGGGGAT 1420 CCRRCTCTGTGTGGGGAT 1420 TGTTGATGGGAT 1420 TGTTGATGGGAT 1420 TGTTGATGGAT 1550 TGTTGAT 1550 TGTTGA	1170 1300 1300 1816HTT 1430 11716HT
#F7181.1-U F7181.1-U	1041 TGGCR 1171 TGCR TGCR TGCR TGCR TGCR TGCR TGCR TGCR	1050 1180 1310 THE	1060 1190 1320 1320 1450 1450 16 HEART FIGURE 1450 16 HEART FIGURE 15 HEART FI	GCGTGAGCA 1070 CCARGTGGC 1200 CCAGGTACCAC 1330 TRITACTIT TR	1080 TCTATTGTTR 1210 RTTTRACART 1340 RRCTGCAGAT RRCTGCAGAT RRCTGCAGAT 1470 ACCTGTCAGAT RCCTGTCAGAT R	1090 1220 1220 ATGTGCTTCT 1350 GTTATGTCCT GTTATGTCCT 1480 PROGRATECTEC PROGRATECTEC PROGRATECTEC REGATECTEC 1510 ATTECGTCCCC	1100 1230 REGERTRETCH CARGITET	1110 1240 CCTGTRCCTGT CCTGTRCCTGC CCTGTRCCTGC CCTGTRCCTGC CTGTRCCTGC CTGTRCCTGC CTGTRCCTGC CTGTRCCTGC CTGTRCCTGC CTGTRCCTGC CTGTRCCTGC CTGTRCATRCGC CTGTRCATRCCC	1120 1250 1250 1250 1250 1250 1250 1250	1130 TRANGECACHE 1260 GCTACCHRAIL GCTACCHRAIL 1390 AGGATT GGAR AGGATT GGAR 1520 GTTACCHRAIL 1520 GTTACCHRAIL 1520 GTTACCHRAIL 1520 GTTACCHRAIL 1520 GTTACCHRAIL 1520 GTTACCHRAIL 1550 GCTCCATCTG	1140 SGGTCRTANCR 1270 THRISCAGUR	1150 1200 176CRETTTI 1200 176CREGRER 1410 CCCCCCCCCCC CCCCCCCCCCCCCCCCCCCCCC	1160 GCTGGCATAGAT 1290 TGTTGGGGGAT TGTTGGGGGAT TGTTGGGGGAT 1420 CCRRCTCTGTGTGGGGAT 1420 TGTTGATGGGAT 1420 TGTTGATGGGAT 1420 TGTTGATGGAT 1550 TGTTGAT 1550 TGTTGA	1170 1300 1300 1816HTT 1430 11716HT

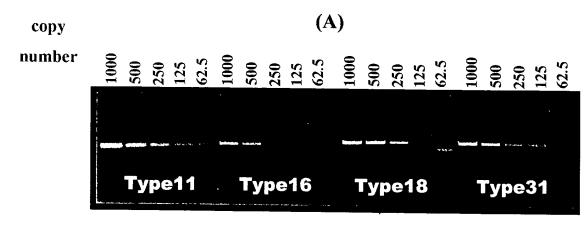
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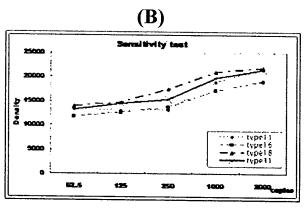
Fig. 6



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Fig. 7





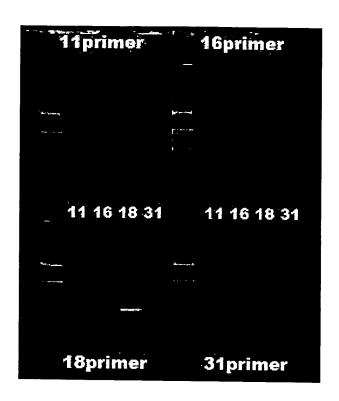
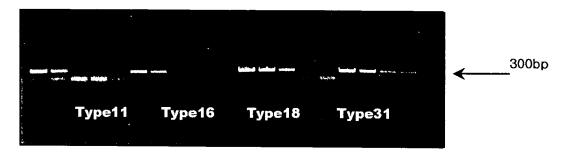
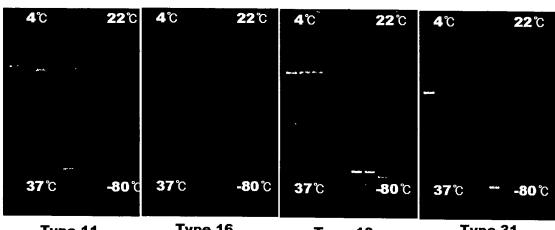


Fig. 9

a. Time point : 0 week



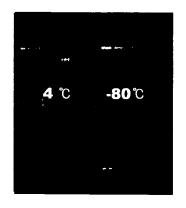
b. Time point: 3 week



Type 16 Type 11 Type 18 Type 31

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Fig. 10



Type11:4 ℃ & -80℃

Y=3.2082X +7596.062 R=0.95

Y=4.219X +8242.484 R=0.97 Type16:4 ℃ & -80 ℃

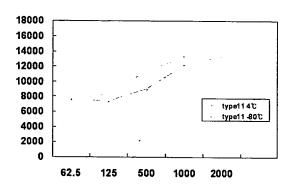
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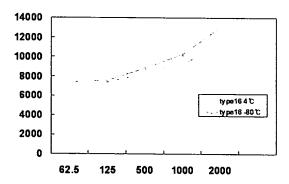
R=0.99

Y=2.926X +7273.275

R=0.99

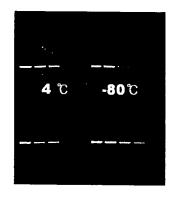
Type11 & Type16





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Fig. 11



Type18:4 ℃ & -80℃

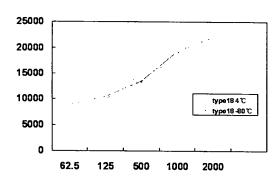
Y=5.705X +10164.36 R=0.95

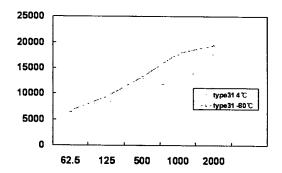
Y=6.7899X +9894.448 R=0.97 **Type31:4 ℃ & -80**℃

Y=4.6447X +8066.789 R=0.94

Y=6.187X + 8781.618 R=0.92

Type18 & Type31





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Fig. 12

